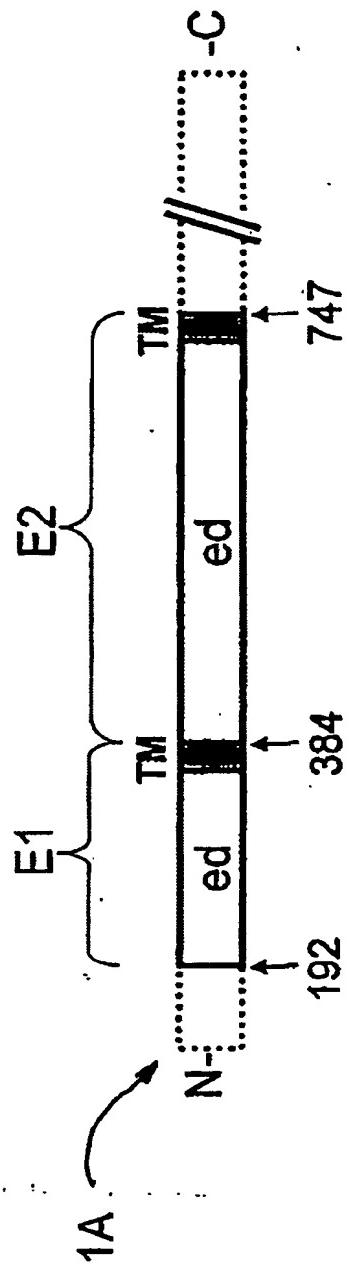


10/528344

1 / 9



TME1: 347-MIAGAHWGVLAGIAYESMVGNWAKVLLVILLFAGVDA-383

TME2: 717-EIVVILLILLADARVCSCILWQMLLISQAEA-746

FIG. 1

10/528344

2 / 9

A 367MIGGAHNGVILAGIAYFMSMVGNWAKVLVVVILFAGVDA₃₆₃, 37 aa, 3861 Da.

B

N°	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	..
aa	M	I	A	G	A	H	W	G	V	L	A	G	I	A	Y	F	S	M	V	..
Seq	ATGATCGCTGGTGCCTCACTGGGGTGTCTGGCTGGTATCGCTTACTTCTATGGT..																			
	1	10	20	30	40	50														
N°	..20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37		
aa	..G	N	W	A	K	V	L	V	V	L	L	F	A	G	V	D	A			
Seq	..GGTAACGGGCTAAAGTTCTGGTTCTGGCTGGCTGGCTGGTGTGACGGCT..																			
	60	70	80	90	100	110														

C

NdeI

5' _GGGAATGCCATATGATCGCTGGTG_ 3'
5' _ATGCCATATGATCGCTGGCTCAGCTGGGTTCTGGCTGGTATCGCTTACITCTATGGTTGGTAAC..
3' _TACGGTATACTAGCGACCACGAGTGAACCCACAAGACCGACCATAGCGAATGAAGAGATAACCAACCATG..

ClaI

TGGGCTAAAGTTCTGGTTCTGGCTGGCTGGTGTGACGGCTTAGATCGATATGC_ 3' 131 bases
.ACCCGATTCAAGACCAACAAGACGACGACAAGCAGCAAGCAGCAACACTGGCAATCTAGCTATAACG_ 5'
3' _ACAACTGGCAATCTAGCTATAACG_ 5'

FIG. 2

10/528344

3 / 9

D
OL11(+): 5'atgccatatgtatcgctggtgctcaactgggtttctggctgtatcgcttacttcttagtttgtaaactggg
OL12(-): 5'gcatatcgatctaagcgtcaacaccaggcgaacacccagaactttagccaggatccaaccatagaa

Cloning in pT7-7:

OL13(+): 5'ggaaatgccatatgtatcgctggtg
OL14(-): 5'gcatatcgatctaaggctcaaca

Cloning in pGEXKT:

OL15(+): 5'ggatccatggaaatacgttgttc (without DP site)
OL17(+): 5'ggatccgaccggatggaaatacgttgttc (with DP site)
OL16(-): 5'gaattcttaaggcttcagcctgag

Cloning in pET32a:

OL18(+): 5'gtgatatactgtatcgctgggtt (hybridizes to the segment 915-932 of pGEXKT)
OL16(-): 5'gaattcttaaggcttcagcctgag

Cloning in pT7-7 of (M)DP-TME1::

OL19 (+) : 5'- CGCATATTGGACCCGATCGGTGCT -3' (Nde I underlined)
OL20 (-) : 5'-GAATTCCTAAGCGTCAACACCAGC-3' (EcoR I underlined)

FIG . 2

101528344

4 / 9

A (M) _{71,7} EYVWILLFILLADARVCSCLMMLISQAEAA₇₄₆

31 aa, 3546 Da.

B

N°	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	..
Aa	M	E	Y	V	V	L	L	F	L	L	A	D	A	R	V	..	
Seq	ATGGAATACTGGTGTCTGCTGCTGGCTGACGCTCGTGT..																
	1	10	20	30	40												

N°	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	..
Aa	..	C	S	C	L	W	M	M	L	L	I	S	Q	A	E	A
Seq	TGCTCTGGCTGTGGATGATGCTGCTGATCTCAGGCTGAGCT..															
	50	60	70	80	90	93										

C

NdeI

5'-CATATGGATAACCTGGTTC 3'

(+) 5'-CATATGGATAACCTGGTGTCTGGCTGCTGGCTGACGCTCGTGT..

(-) 3'-GTATACCTTATGCAACAGAACGACAAGGGACGACCGACTGGAGCACAA..

Hind III

..TGCTCTGGCTGTGGATGATGCTGCTGATCTCAGGCTGAAGCTT-3' 117 bp
 ..ACGAGAACGGACACCTACTACGACGACTAGAGAGTCCGACTTCGAATTCAA-5'
 3' - GACTAGAGAGTCCGACTTCGAATTCAA-5'

FIG. 3

10/528344

5 / 9

D
OL21(+): 5'catatggaaatacgttgtttctgtctggctgacgctcggttttgcctgtggat
OL22(-): 5'aagctaaggcttcagccctgagagatcagcagcatccacaggcaagaaacac

Cloning in pT7-7:

OL23(+): 5'catatggaaatacgttgttc
OL24(-): 5'aagctaaggcttcagccctgagagatcag

Cloning in pGEXKT:

OL25(+): 5'ggatccgaatacgttgttc (without DP site)
OL27(+): 5'ggatccgaccggaaatacgttgttc (with DP site)
OL26(-): 5'gaattttaaggcttcagccctgagagatcag

Cloning in pET32a:

OL18(+): 5'gtgatatatgtatctgttgttgtgtt (hybridizes to the segment 915-932 of pGEXKT)
OL26(-): 5'gaattttaaggcttcagccctgagagatcag

Cloning in pT7-7 of (M)DP-TME2:

OL28 (+) : 5'- CGCATATGGACCCGGAAATAACGTTGTTC-3' (Nde I underlined)
OL29 (-) : 5'-CAGAATTCTTAAGCTTGAGAG-3' (EcoR I underlined)

FIG. 3

10/528344

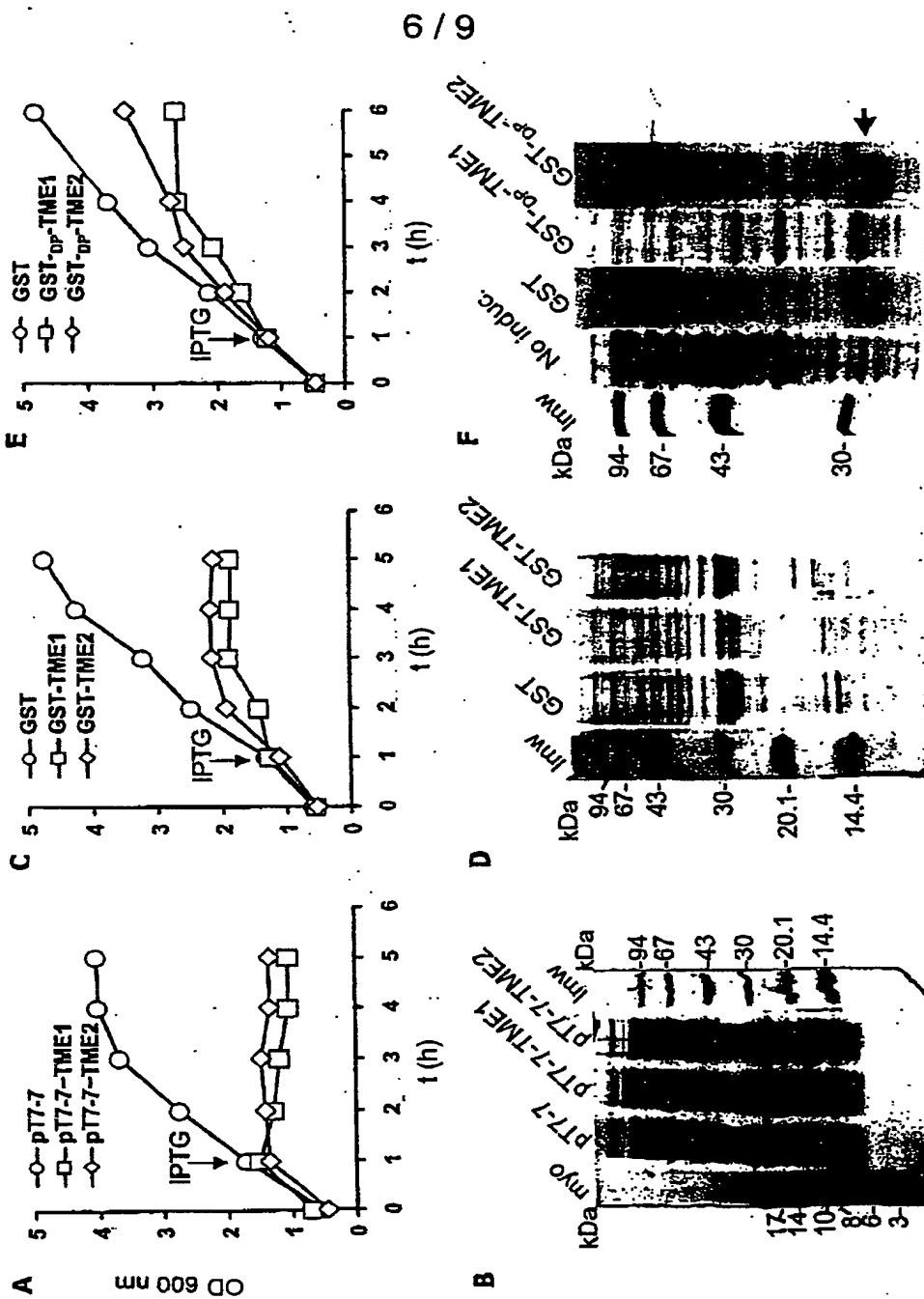


FIG. 4

10/528344

7 / 9

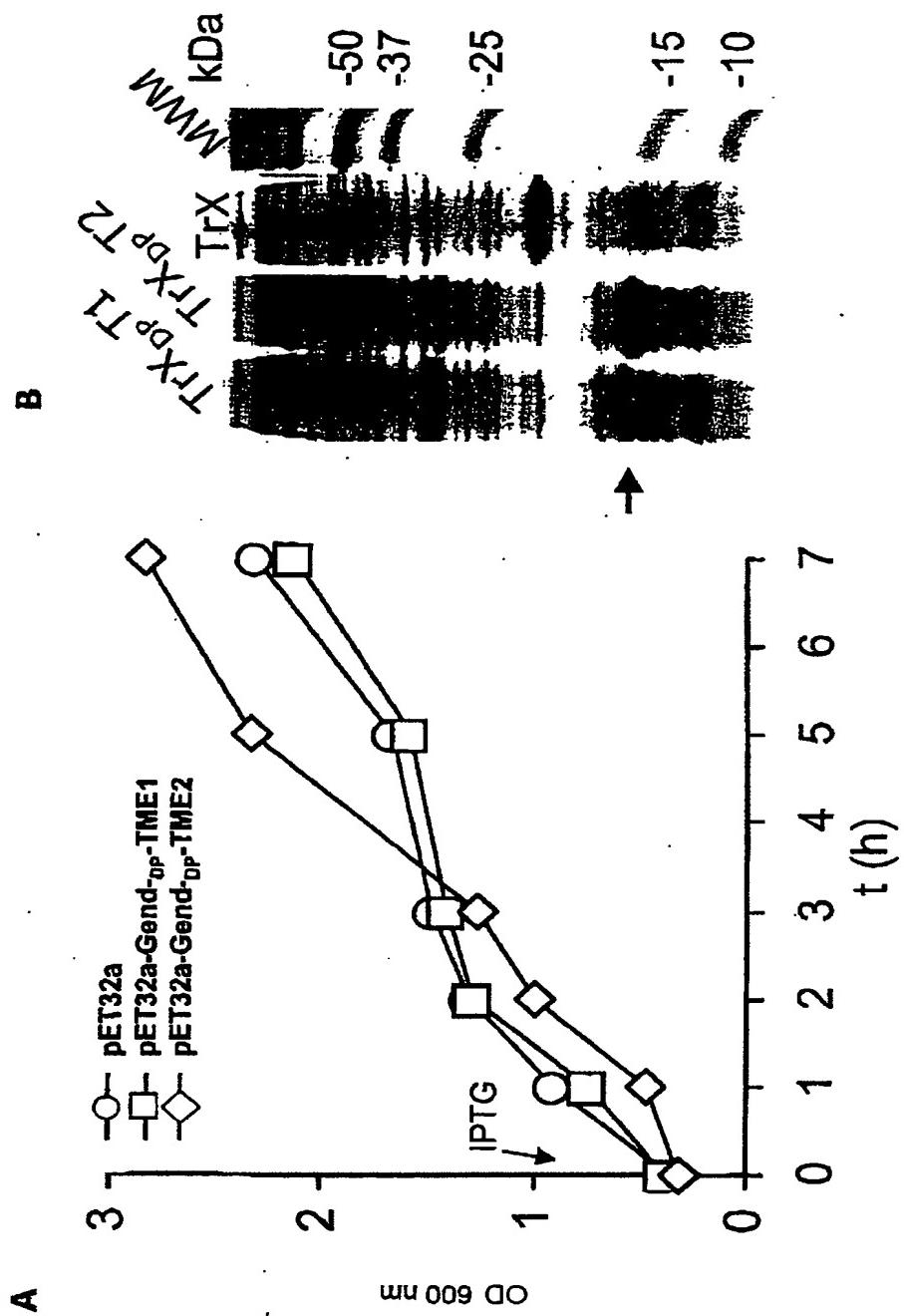


FIG. 5

10/528344

8 / 9

GST :
 MSPILGYWKIGLVQQPTRLLLEKYEELYERDEGDKWRNKKFELGLEFPNLPPYYIDGDVKLTQSMAIIRYI
 ADKHNMLGGCPKERAETSMLEGAVLDIYGVSRIAYSKDFETLKVDFESKLPEMLKMFEDRLCHKTLYNGDHVTH
 PDFMFLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAMPLQGWQATFGGGDHPPKSDLSGGG
GGLVPRGS/PGIHRD

GST-TME2 :
 MSPILGYWKIGLVQQPTRLLLEKYEELYERDEGDKWRNKKFELGLEFPNLPPYYIDGDVKLTQSMAIIRYIA
 DKHNMLGGCPKERAETSMLEGAVLDIYGVSRIAYSKDFETLKVDFESKLPEMLKMFEDRLCHKTLYNGDHVTHPD
 FMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAMPLQGWQATFGGGDHPPKSDLSGGGCGC
VPRGS/EYVVNLTTTADARYCSCLNWMMILLISQAEAA

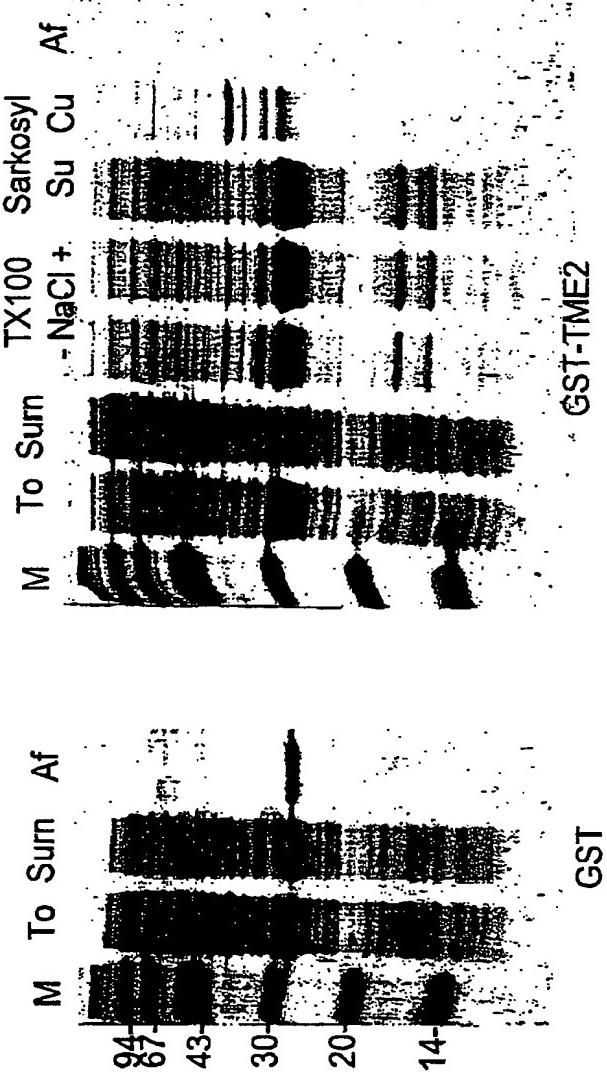


FIG. 6

10/528344

9 / 9

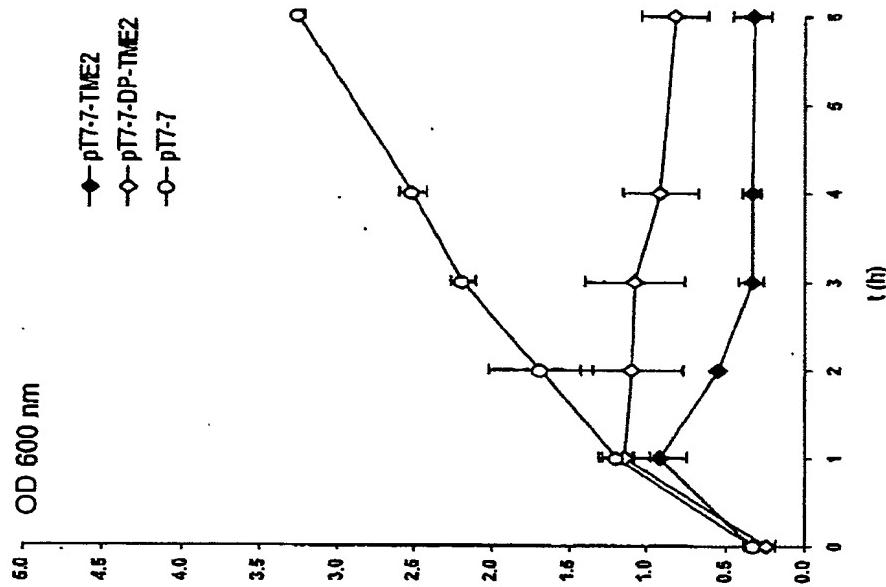


FIG. 7B

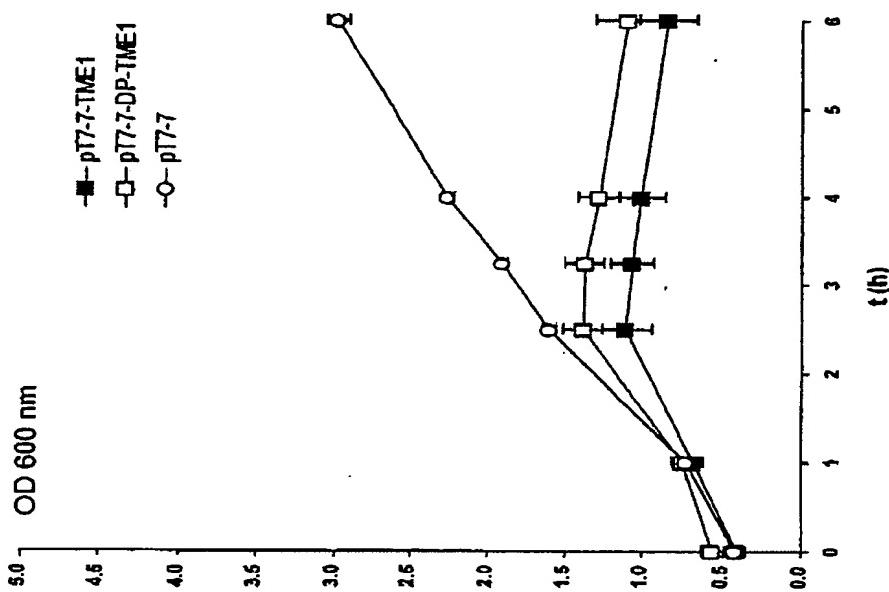


FIG. 7A